

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 09/445,223A  
Source: IFW/16  
Date Processed by STIC: 5/6/05

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 05/06/2005

PATENT APPLICATION: US/09/445,223A

TIME: 15:22:14

Input Set : A:\sequence listing.txt

Output Set: N:\CRF4\05062005\I445223A.raw

CELL

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3 <110> APPLICANT: WALLACH, David
4     BOLDIN, Mark
5     MALININ, Nikolai
7 <120> TITLE OF INVENTION: MODULATORS OF INTRACELLULAR INFLAMMATION, CELL DEATH AND
CELL
8     SURVIVAL PATHWAYS
10 <130> FILE REFERENCE: WALLACH=24
12 <140> CURRENT APPLICATION NUMBER: 09/445,223A
13 <141> CURRENT FILING DATE: 1999-12-06
15 <150> PRIOR APPLICATION NUMBER: IL 121011
16 <151> PRIOR FILING DATE: 1997-06-05
18 <150> PRIOR APPLICATION NUMBER: IL 121199
19 <151> PRIOR FILING DATE: 1997-06-30
21 <150> PRIOR APPLICATION NUMBER: IL 121746
22 <151> PRIOR FILING DATE: 1997-09-11
24 <160> NUMBER OF SEQ ID NOS: 3
26 <170> SOFTWARE: PatentIn version 3.3
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 540
30 <212> TYPE: PRT
31 <213> ORGANISM: Homo sapiens
33 <400> SEQUENCE: 1
35 Met Asn Gly Glu Ala Ile Cys Ser Ala Leu Pro Thr Ile Pro Tyr His
36 1           5           10           15
39 Lys Leu Ala Asp Leu Arg Tyr Leu Ser Arg Gly Ala Ser Gly Thr Val
40           20           25           30
43 Ser Ser Ala Arg His Ala Asp Trp Arg Val Gln Val Ala Val Lys His
44           35           40           45
47 Leu His Ile His Thr Pro Leu Leu Asp Ser Glu Arg Lys Asp Val Leu
48           50           55           60
51 Arg Glu Ala Glu Ile Leu His Lys Ala Arg Phe Ser Tyr Ile Phe Pro
52 65           70           75           80
55 Ile Leu Gly Ile Cys Asn Glu Pro Glu Phe Leu Gly Ile Val Thr Glu
56           85           90           95
59 Tyr Met Pro Asn Gly Ser Leu Asn Glu Leu Leu His Arg Lys Thr Glu
60           100          105          110
63 Tyr Pro Asp Val Ala Trp Pro Leu Arg Phe Arg Ile Leu His Glu Ile
64           115          120          125
67 Ala Leu Gly Val Asn Tyr Leu His Asn Met Thr Pro Leu Leu His
68           130          135          140
71 His Asp Leu Lys Thr Gln Asn Ile Leu Leu Asp Asn Glu Phe His Val
72 145          150          155          160
75 Lys Ile Ala Asp Phe Gly Leu Ser Lys Trp Arg Met Met Ser Leu Ser
76           165          170          175

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79 Gln Ser Arg Ser Ser Lys Ser Ala Pro Glu Gly Gly Thr Ile Ile Tyr
80          180          185          190
83 Met Pro Pro Glu Asn Tyr Glu Pro Gly Gln Lys Ser Arg Ala Ser Ile
84          195          200          205
87 Lys His Asp Ile Tyr Ser Tyr Ala Val Ile Thr Trp Glu Val Leu Ser
88          210          215          220
91 Arg Lys Gln Pro Phe Glu Asp Val Thr Asn Pro Leu Gln Ile Met Tyr
92 225          230          235          240
95 Ser Val Ser Gln Gly His Arg Pro Val Ile Asn Glu Glu Ser Leu Pro
96          245          250          255
99 Tyr Asp Ile Pro His Arg Ala Arg Met Ile Ser Leu Ile Glu Ser Gly
100          260          265          270
103 Trp Ala Gln Asn Pro Asp Glu Arg Pro Ser Phe Leu Lys Cys Leu Ile
104          275          280          285
107 Glu Leu Glu Pro Val Leu Arg Thr Phe Glu Glu Ile Thr Phe Leu Glu
108          290          295          300
111 Ala Val Ile Gln Leu Lys Lys Thr Lys Leu Gln Ser Val Ser Ser Ala
112 305          310          315          320
115 Ile His Leu Cys Asp Lys Lys Lys Met Glu Leu Ser Leu Asn Ile Pro
116          325          330          335
119 Val Asn His Gly Pro Gln Glu Glu Ser Cys Gly Ser Ser Gln Leu His
120          340          345          350
123 Glu Asn Ser Gly Ser Pro Glu Thr Ser Arg Ser Leu Pro Ala Pro Gln
124          355          360          365
127 Asp Asn Asp Phe Leu Ser Arg Lys Ala Gln Asp Cys Tyr Phe Met Lys
128          370          375          380
131 Leu His His Cys Pro Gly Asn His Ser Trp Asp Ser Thr Ile Ser Gly
132 385          390          395          400
135 Ser Gln Arg Ala Ala Phe Cys Asp His Lys Thr Thr Pro Cys Ser Ser
136          405          410          415
139 Ala Ile Ile Asn Pro Leu Ser Thr Ala Gly Asn Ser Glu Arg Leu Gln
140          420          425          430
143 Pro Gly Ile Ala Gln Gln Trp Ile Gln Ser Lys Arg Glu Asp Ile Val
144          435          440          445
147 Asn Gln Met Thr Glu Ala Cys Leu Asn Gln Ser Leu Asp Ala Leu Leu
148          450          455          460
151 Ser Arg Asp Leu Ile Met Lys Glu Asp Tyr Glu Leu Val Ser Thr Lys
152 465          470          475          480
155 Pro Thr Arg Thr Ser Lys Val Arg Gln Leu Leu Asp Thr Thr Asp Ile
156          485          490          495
159 Gln Gly Glu Glu Phe Ala Lys Val Ile Val Gln Lys Leu Lys Asp Asn
160          500          505          510
163 Lys Gln Met Gly Leu Gln Pro Tyr Pro Glu Ile Leu Val Val Ser Arg
164          515          520          525
167 Ser Pro Ser Leu Asn Leu Leu Gln Asn Lys Ser Met
168          530          535          540
171 <210> SEQ ID NO: 2
172 <211> LENGTH: 2098
173 <212> TYPE: DNA

```

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```

174 <213> ORGANISM: Homo sapiens
176 <400> SEQUENCE: 2
177 ggccattatg gatggatggg cggcgctacg gcgttggcac cagtctctag aaaagaagtc      60
179 agctctgggt cggagaagca gcggctggcg tgggccaatcc ggggaatggg cgccctcgtg      120
181 acctagtgtt gcggggcaaa aagggtcttg ccggcctcgc tcgtgcaggg gcgtatctgg      180
183 gcgcctgagc gcggcggtgg agccttggga gccgcgcag cagggggcac acccggaacc      240
185 ggctgagcg cccgggacca tgaacgggga ggccaatcgc agcgccctgc ccaccattcc      300
187 ctaccacaaa ctgcgcgacc tgcgtacct gagcgcggc gcctctggca ctgtgtcgtc      360
189 cggccggcac gcagactggc gcgtccaggt ggccgtgaag cacctgcaca tccacactcc      420
191 gctgctcgac agtgaagaa aggatgtttt aagagaagct gaaattttac acaaagctag      480
193 atttagttac atttttccaa ttttgggaat ttgcaatgag cctgaatttt tgggaatagt      540
195 tactgaatac atgccaaatg gatcattaaa tgaactccta cataggaaaa ctgaatatcc      600
197 tgatgttgct tggccattga gatttcgcat cctgcatgaa attgcccttg gtgtaaatga      660
199 cctgcacaat atgactcctc ctttacttca tcatgacttg aagactcaga atatcttatt      720
201 ggacaatgaa tttcatgtta agattgcaga ttttggttta tcaaagtggc gcatgatgtc      780
203 cctctcacag tcacgaagta gcaaactcgc accagaagga gggacaatta tttatatgcc      840
205 acctgaaaac tatgaacctg gacaaaaatc aagggccagt atcaagcacg atatatatag      900
207 ctatgcagtt atcacatggg aagtgttatt cagaaaacag ccttttgaag atgtcaccaa      960
209 tcctttgcag ataatgtata gtgtgtcaca aggacatcga cctgttatta atgaagaaag     1020
211 tttgccatat gatatacctc accgagcacg tatgatctct ctaatagaaa gtggatgggc     1080
213 acaaaatcca gatgaaagac catctttctt aaaatgttta atagaacttg aaccagtttt     1140
215 gagaacattt gaagagataa cttttcttga agctgttatt cagctaaaga aaacaaagtt     1200
217 acagagtgtt tcaagtgcc ttcacctatg tgacaagaag aaaatggaat tatctctgaa     1260
219 catacctgta aatcatggtc cacaagagga atcatgtgga tcctctcagc tccatgaaaa     1320
221 tagtggttct cctgaaactt caaggctcct gccagctcct caagacaatg attttttatc     1380
223 tagaaaagct caagactgtt attttatgaa gctgcatcac tgtcctggaa atcacagttg     1440
225 ggatagcacc atttctggat ctcaaagggc tgcattctgt gatcacaaga cactccatg     1500
227 ctcttcagca ataataaatc cactctcaac tgcaggaaac tcagaacgtc tgcagcctgg     1560
229 tatagcccag cagtggatcc agagcaaaaag ggaagacatt gtgaaccaa tgacagaagc     1620
231 ctgccttaac cagtcgctag atgcccttct gtccagggac ttgatcatga aagaggacta     1680
233 tgaacttggt agtaccaagc ctacaaggac ctcaaaagtc agacaattac tagacactac     1740
235 tgacatccaa ggagaagaat ttgccaaagt tatagtacaa aaattgaaag ataacaaaca     1800
237 aatgggtctt cagccttacc cggaaatact tgtggtttct agatcaccat ctttaaattt     1860
239 acttcaaaat aaaagcatgt aagtgactgt ttttcaagaa gaaatgtgt tcataaaagg     1920
241 atatttatat ctctgttgc ttgacttttt ttatataaaa tccgtgagta ttaaagcttw     1980
243 awwraargkt ctttsrktaa atattagtct ccctccatga cactgcagta ttttttttaa     2040
245 ttaatacaag taaaaagttg aatttgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa     2098
248 <210> SEQ ID NO: 3
249 <211> LENGTH: 4
250 <212> TYPE: PRT
251 <213> ORGANISM: Artificial
253 <220> FEATURE:
254 <223> OTHER INFORMATION: Synthetic
257 <220> FEATURE:
258 <221> NAME/KEY: misc_feature
259 <222> LOCATION: (1)..(1)
260 <223> OTHER INFORMATION: Residue at postion 1 is modified by an acetyl group.
262 <220> FEATURE:
263 <221> NAME/KEY: misc_feature

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264 <222> LOCATION: (4)..(4)  
265 <223> OTHER INFORMATION: Residue at postion 4 is modified by  
266 a-(4-methyl-coumaryl-7-amide).  
268 <220> FEATURE:  
269 <221> NAME/KEY: misc\_feature  
270 <222> LOCATION: (4)..(4)  
271 <223> OTHER INFORMATION: Residue at postion 4 is modified by an AC-DEVD-AMC group.  
273 <400> SEQUENCE: 3  
275 Asp Glu Val Asp  
276 1

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 05/06/2005  
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3

**VERIFICATION SUMMARY**

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